==========

Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2011; month=6; day=23; hr=8; min=33; sec=51; ms=192;]

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Reviewer Comments:

<210> 1

<211> 522

<212> PRT

<213> Saccharomyces cerevisiae protein disulphide isomerase precursor

The above "<213>" response is invalid, per 1.823 of the Sequence Rules. The only valid "<213>" responses are: the Genus species (just the Genus species) of the organism, "Artificial Sequence", or "Unknown". If either "Artificial Sequence" or if "Unknown", a mandatory explanation in a "<220>-<223>" section is required; please clearly indicate the source of the genetic material. This type of error also appears in subsequent sequences.

<210> 3

<211> 8

<212> PRT

<213> Saccharomyces cerevisiae alternative protein disulphide isomerase amino acids 506-513

<400> 3

Glu Ala Asp Ala Glu Ala Glu Ala
1   5

Regarding the above "<213>" response: not only is it invalid, but the line exceeds the Sequence Rules' required 72-character line limit. This error occurs throughout the sequence listing. Please ensure that all lines in the sequence listing do not exceed 72 characters.

To correct the sequence listing errors noted in this report - The

recommended method for correction of errors is to access the sequence listing working file using the software program in which the listing was originally prepared, e.g., the project file in PatentIn, make any necessary corrections within that program, then generate a new sequence listing file. Use of a word processing program to correct errors directly in the original sequence listing file is strongly discouraged, since such programs often introduce unintended changes to the sequence listing, rendering the listing unacceptable. When the working file or original program is not available for correction, then use of a common or plain text-only editor, such as NotePad, to edit the original sequence listing file may suffice.

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Validated By CRFValidator v 1.0.3

Application No: 10584424 Version No: 1.0

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Output Set:

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Finished: 2011-06-14 14:13:48.821
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 607 ms
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Total Errors: 0
No. of SeqIDs Defined: 80
Actual SeqID Count: 80

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W 213	Artificial or Unknown found in <213> in SEQ ID (10)
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Output Set:

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Actual SeqID Count: 80

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W 213	Artificial or Unknown found in <213> in SEQ ID (29)
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Sleep, Darrell
Shuttleworth, Gillian
Finnis, Christopher John Arthur

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<140> 10584424
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<150> PCT/GB2004/005462
<151> 2004-12-23

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<210> 1
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<213> Saccharomyces cerevisiae protein disulphide isomerase precursor

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35 40 45

His Asp Leu Val Leu Ala Glu Phe Phe Ala Pro Trp Cys Gly His Cys
50 55 60

Lys Asn Met Ala Pro Glu Tyr Val Lys Ala Ala Glu Thr Leu Val Glu
65 70 75 80

Lys Asn Ile Thr Leu Ala Gln Ile Asp Cys Thr Glu Asn Gln Asp Leu
85 90 95

Cys Met Glu His Asn Ile Pro Gly Phe Pro Ser Leu Lys Ile Phe Lys
100 105 110

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Asn Ser Asp Val Asn Asn Ser Ile Asp Tyr Glu Gly Pro Arg Thr Ala
        115                 120                 125

Glu Ala Ile Val Gln Phe Met Ile Lys Gln Ser Gln Pro Ala Val Ala
    130                 135                 140

Val Val Ala Asp Leu Pro Ala Tyr Leu Ala Asn Glu Thr Phe Val Thr
145                 150                 155                 160

Pro Val Ile Val Gln Ser Gly Lys Ile Asp Ala Asp Phe Asn Ala Thr
                165                 170                 175

Phe Tyr Ser Met Ala Asn Lys His Phe Asn Asp Tyr Asp Phe Val Ser
            180                 185                 190

Ala Glu Asn Ala Asp Asp Asp Phe Lys Leu Ser Ile Tyr Leu Pro Ser
        195                 200                 205

Ala Met Asp Glu Pro Val Val Tyr Asn Gly Lys Lys Ala Asp Ile Ala
    210                 215                 220

Asp Ala Asp Val Phe Glu Lys Trp Leu Gln Val Glu Ala Leu Pro Tyr
225                 230                 235                 240

Phe Gly Glu Ile Asp Gly Ser Val Phe Ala Gln Tyr Val Glu Ser Gly
                245                 250                 255

Leu Pro Leu Gly Tyr Leu Phe Tyr Asn Asp Glu Glu Glu Leu Glu Glu
            260                 265                 270

Tyr Lys Pro Leu Phe Thr Glu Leu Ala Lys Lys Asn Arg Gly Leu Met
        275                 280                 285

Asn Phe Val Ser Ile Asp Ala Arg Lys Phe Gly Arg His Ala Gly Asn
    290                 295                 300

Leu Asn Met Lys Glu Gln Phe Pro Leu Phe Ala Ile His Asp Met Thr
305                 310                 315                 320

Glu Asp Leu Lys Tyr Gly Leu Pro Gln Leu Ser Glu Glu Ala Phe Asp
                325                 330                 335
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Glu Leu Ser Asp Lys Ile Val Leu Glu Ser Lys Ala Ile Glu Ser Leu
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Val Lys Asp Phe Leu Lys Gly Asp Ala Ser Pro Ile Val Lys Ser Gln
355 360 365

Glu Ile Phe Glu Asn Gln Asp Ser Ser Val Phe Gln Leu Val Gly Lys
370 375 380

Asn His Asp Glu Ile Val Asn Asp Pro Lys Lys Asp Val Leu Val Leu
385 390 395 400

Tyr Tyr Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala Pro Thr Tyr
405 410 415

Gln Glu Leu Ala Asp Thr Tyr Ala Asn Ala Thr Ser Asp Val Leu Ile
420 425 430

Ala Lys Leu Asp His Thr Glu Asn Asp Val Arg Gly Val Val Ile Glu
435 440 445

Gly Tyr Pro Thr Ile Val Leu Tyr Pro Gly Gly Lys Lys Ser Glu Ser
450 455 460

Val Val Tyr Gln Gly Ser Arg Ser Leu Asp Ser Leu Phe Asp Phe Ile
465 470 475 480

Lys Glu Asn Gly His Phe Asp Val Asp Gly Lys Ala Leu Tyr Glu Glu
485 490 495

Ala Gln Glu Lys Ala Ala Glu Glu Ala Asp Ala Asp Ala Glu Leu Ala
500 505 510

Asp Glu Glu Asp Ala Ile His Asp Glu Leu
515 520

<210> 2
<211> 530
<212> PRT
<213> Saccharomyces cerevisiae alternative protein disulphide isomerase

<400> 2

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Ala Val Val Lys Leu Ala Thr Asp Ser Phe Asn Glu Tyr Ile Gln Ser
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His Asp Leu Val Leu Ala Glu Phe Phe Ala Pro Trp Cys Gly His Cys
    50                  55                  60

Lys Asn Met Ala Pro Glu Tyr Val Lys Ala Ala Glu Thr Leu Val Glu
65                  70                  75                  80

Lys Asn Ile Thr Leu Ala Gln Ile Asp Cys Thr Glu Asn Gln Asp Leu
                85                  90                  95

Cys Met Glu His Asn Ile Pro Gly Phe Pro Ser Leu Lys Ile Phe Lys
            100                 105                 110

Asn Arg Asp Val Asn Asn Ser Ile Asp Tyr Glu Gly Pro Arg Thr Ala
        115                 120                 125

Glu Ala Ile Val Gln Phe Met Ile Lys Gln Ser Gln Pro Ala Val Ala
    130                 135                 140

Val Val Ala Asp Leu Pro Ala Tyr Leu Ala Asn Glu Thr Phe Val Thr
145                 150                 155                 160

Pro Val Ile Val Gln Ser Gly Lys Ile Asp Ala Asp Phe Asn Ala Thr
                165                 170                 175

Phe Tyr Ser Met Ala Asn Lys His Phe Asn Asp Tyr Asp Phe Val Ser
            180                 185                 190

Ala Glu Asn Ala Asp Asp Asp Phe Lys Leu Ser Ile Tyr Leu Pro Ser
        195                 200                 205

Ala Met Asp Glu Pro Val Val Tyr Asn Gly Lys Lys Ala Asp Ile Ala
    210                 215                 220

Asp Ala Asp Val Phe Glu Lys Trp Leu Gln Val Glu Ala Leu Pro Tyr
225                 230                 235                 240
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Phe Gly Glu Ile Asp Gly Ser Val Phe Ala Gln Tyr Val Glu Ser Gly
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Leu Pro Leu Gly Tyr Leu Phe Tyr Asn Asp Glu Glu Glu Leu Glu Glu
260 265 270

Tyr Lys Pro Leu Phe Thr Glu Leu Ala Lys Lys Asn Arg Gly Leu Met
275 280 285

Asn Phe Val Ser Ile Asp Ala Arg Lys Phe Gly Arg His Ala Gly Asn
290 295 300

Leu Asn Met Lys Glu Gln Phe Pro Leu Phe Ala Ile His Asp Met Thr
305 310 315 320

Glu Asp Leu Lys Tyr Gly Leu Pro Gln Leu Ser Glu Glu Ala Phe Asp
325 330 335

Glu Leu Ser Asp Lys Ile Val Leu Glu Ser Lys Ala Ile Glu Ser Leu
340 345 350

Val Lys Asp Phe Leu Lys Gly Asp Ala Ser Pro Ile Val Lys Ser Gln
355 360 365

Glu Ile Phe Glu Asn Gln Asp Ser Ser Val Phe Gln Leu Val Gly Lys
370 375 380

Asn His Asp Glu Ile Val Asn Asp Pro Lys Lys Asp Val Leu Val Leu
385 390 395 400

Tyr Tyr Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala Pro Thr Tyr
405 410 415

Gln Glu Leu Ala Asp Thr Tyr Ala Asn Ala Thr Ser Asp Val Leu Ile
420 425 430

Ala Lys Leu Asp His Thr Glu Asn Asp Val Arg Gly Val Val Ile Glu
435 440 445

Gly Tyr Pro Thr Ile Val Leu Tyr Pro Gly Gly Lys Lys Ser Glu Ser
450 455 460

Val Val Tyr Gln Gly Ser Arg Ser Leu Asp Ser Leu Phe Asp Phe Ile
465 470 475 480

Lys Glu Asn Gly His Phe Asp Val Asp Gly Lys Ala Leu Tyr Glu Glu
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Ala Gln Glu Lys Ala Ala Glu Glu Ala Glu Ala Asp Ala Glu Ala Glu
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<210> 3
<211> 8
<212> PRT
<213> Saccharomyces cerevisiae alternative protein disulphide isomerase amino acids 506-513

<400> 3

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<210> 4
<211> 642
<212> PRT
<213> Saccharomyces cerevisiae SSA1 protein

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20 25 30

Asn Arg Thr Thr Pro Ser Phe Val Ala Phe Thr Asp Thr Glu Arg Leu
35 40 45

Ile Gly Asp Ala Ala Lys Asn Gln Ala Ala Met Asn Pro Ser Asn Thr
50 55 60

Val Phe Asp Ala Lys Arg Leu Ile Gly Arg Asn Phe Asn Asp Pro Glu
65 70 75 80

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Val Gln Ala Asp Met Lys His Phe Pro Phe Lys Leu Ile Asp Val Asp
                85                  90                  95

Gly Lys Pro Gln Ile Gln Val Glu Phe Lys Gly Glu Thr Lys Asn Phe
            100                 105                 110

Thr Pro Glu Gln Ile Ser Ser Met Val Leu Gly Lys Met Lys Glu Thr
        115                 120                 125

Ala Glu Ser Tyr Leu Gly Ala Lys Val Asn Asp Ala Val Val Thr Val
    130                 135                 140

Pro Ala Tyr Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp Ala Gly
145                 150                 155                 160

Thr Ile Ala Gly Leu Asn Val Leu Arg Ile Ile Asn Glu Pro Thr Ala
                165                 170                 175

Ala Ala Ile Ala Tyr Gly Leu Asp Lys Lys Gly Lys Glu Glu His Val
            180                 185                 190

Leu Ile Phe Asp Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu Phe
        195                 200                 205

Ile Glu Asp Gly Ile Phe Glu Val Lys Ala Thr Ala Gly Asp Thr His
    210                 215                 220

Leu Gly Gly Glu Asp Phe Asp Asn Arg Leu Val Asn His Phe Ile Gln
225                 230                 235                 240

Glu Phe Lys Arg Lys Asn Lys Lys Asp Leu Ser Thr Asn Gln Arg Ala
                245                 250                 255

Leu Arg Arg Leu Arg Thr Ala Cys Glu Arg Ala Lys Arg Thr Leu Ser
            260                 265                 270

Ser Ser Ala Gln Thr Ser Val Glu Ile Asp Ser Leu Phe Glu Gly Ile
        275                 280                 285

Asp Phe Tyr Thr Ser Ile Thr Arg Ala Arg Phe Glu Glu Leu Cys Ala
    290                 295                 300
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Asp Leu Phe Arg Ser Thr Leu Asp Pro Val Glu Lys Val Leu Arg Asp
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Ala Lys Leu Asp Lys Ser Gln Val Asp Glu Ile Val Leu Val Gly Gly
                325                 330                 335

Ser Thr Arg Ile Pro Lys Val Gln Lys Leu Val Thr Asp Tyr Phe Asn
            340                 345                 350

Gly Lys Glu Pro Asn Arg Ser Ile Asn Pro Asp Glu Ala Val Ala Tyr
        355                 360                 365

Gly Ala Ala Val Gln Ala Ala Ile Leu Thr Gly Asp Glu Ser Ser Lys
    370                 375                 380

Thr Gln Asp Leu Leu Leu Leu Asp Val Ala Pro Leu Ser Leu Gly Ile
385                 390                 395                 400

Glu Thr Ala Gly Gly Val Met Thr Lys Leu Ile Pro Arg Asn Ser Thr
                405                 410                 415

Ile Ser Thr Lys Lys Phe Glu Ile Phe Ser Thr Tyr Ala Asp Asn Gln
            420                 425                 430

Pro Gly Val Leu Ile Gln Val Phe Glu Gly Glu Arg Ala Lys Thr Lys
        435                 440                 445

Asp Asn Asn Leu Leu Gly Lys Phe Glu Leu Ser Gly Ile Pro Pro Ala
    450                 455                 460

Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Val Asp Ser Asn
465                 470                 475                 480

Gly Ile Leu Asn Val Ser Ala Val Glu Lys Gly Thr Gly Lys Ser Asn
                485                 490                 495

Lys Ile Thr Ile Thr Asn Asp Lys Gly Arg Leu Ser Lys Glu Asp Ile
            500                 505                 510

Glu Lys Met Val Ala Glu Ala Glu Lys Phe Lys Glu Glu Asp Glu Lys
        515                 520                 525
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Glu Ser Gln Arg Ile Ala Ser Lys Asn Gln Leu Glu Ser Ile Ala Tyr
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Ser Leu Lys Asn Thr Ile Ser Glu Ala Gly Asp Lys Leu Glu Gln Ala
545 550 555 560

Asp Lys Asp Thr Val Thr Lys Lys Ala Glu Glu Thr Ile Ser Trp Leu
565 570 575

Asp Ser Asn Thr Thr Ala Ser Lys Glu Glu Phe Asp Asp Lys Leu Lys
580 585 590

Glu Leu Gln Asp Ile Ala Asn Pro Ile Met Ser Lys Leu Tyr Gln Ala
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Gly Gly Ala Pro Gly Gly Ala Ala Gly Gly Ala Pro Gly Gly Phe Pro
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Gly Gly Ala Pro Pro Ala Pro Glu Ala Glu Gly Pro Thr Val Glu Glu
625 630 635 640

Val Asp

<210> 5
<211> 1929
<212> DNA
<213> Saccharomyces cerevisiae SSA1 coding sequence

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accattgctg gtttgaatgt cttgcgtatt attaacgaac ctaccgccgc tgccattgct 540

tacggtttgg acaagaaggg taaggaagaa cacgtcttga ttttcgactt gggtggtggt 600

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